> This Raw Listing contains the General Information
> Section and up to first 5 pages.

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 1    <110> APPLICANT: Novak, Rodger
 2          Toumanen, Elaine
 3    <120> TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
 4    <130> FILE REFERENCE: 1340-1-016N1
 5    <140> CURRENT APPLICATION NUMBER: US/09/305,984B
 6    <141> CURRENT FILING DATE: 1999-05-05
 7    <150> EARLIER APPLICATION NUMBER: 60/084,399          ENTERED
 8    <151> EARLIER FILING DATE: 1998-05-06
 9    <150> EARLIER APPLICATION NUMBER: 09/305,984
10    <151> EARLIER FILING DATE: 1999-05-05
11    <160> NUMBER OF SEQ ID NOS: 76
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16    <213> ORGANISM: Streptococcus pneumoniae
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28                        20                  25
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30    <211> LENGTH: 75
31    <212> TYPE: DNA
32    <213> ORGANISM: Artificial Sequence
33    <220> FEATURE:
34    <223> OTHER INFORMATION: Description of Artificial Sequence: Encodes
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50                         20               25
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60            gcaagagacg ctaat                                                 75
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63     <212> TYPE: PRT
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72                         20               25
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74     <211> LENGTH: 42
75     <212> TYPE: DNA
76     <213> ORGANISM: Streptococcus pneumoniae
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85             1           5                  10
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87     <211> LENGTH: 33
88     <212> TYPE: DNA
89     <213> ORGANISM: Streptococcus pneumoniae
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105          aaaaggccag caagagacta taat                                        84
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114                         20                  25
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118    <213> ORGANISM: Streptococcus pneumoniae
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122          cgtcaggaaa ccattggtca aaaggcaaca gccattgccc agtccctaga agggaaagat 180
123          aggcagagta tcgagcaagt gttagacttg tattcccaga ctagtgatat caaggggacc 240
124          gtcaaaggtg agatgaccga ggacaagtta gaagtcaagg acagtcttcc tctggacaca 300
125          gaccgccaga caacctctct ctttattgag gagcgcgagg tgaaaacgca agacggtggt 360
126          actatgattc tccagtttct agcttccatg gatttacaaa aggaagcgga gcaaatcagt 420
127          ctccagtttc ttccctatac cttgctggcc tcctttctga tttccctttt ggtggcctac 480
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129          atggacctgg attcccaagt gcgattgcgc gtggattcta aggatgagat aggtaatctc 600
130          aaggaacaaa tcaatagcct ctaccagcat ctcttgactg ttattgcgga cttgcatgaa 660
131          aagaatgaag ccattctcca gctggagaag atgaaggtcg aattcctacg aggagcttct 720
132          catgaattga aaacaccgct ggctagtttg aaaatcctaa tcgaaaatat gagagagaat 780
133          atcggtcgtt ataaggatag agaccagtat ctgggagttg ccttggggat tgtggatgaa 840
134          ctcaatcacc atgttctgca gatactttcc ctctcttctg tgcaggaatt gcgagatgat 900
135          agggaaacaa ttgacctcct ccagatgacg caaaatctgg tcaaagatta tgccttgcta 960
136          gccaaggaaa gagagctcca gatagacaat agtttgaccc atcagcaggc ttatctaaac 1020
137          ccatcagtta tgaagttgat tctttctaat ctcatcagca atgccattaa gcactctgtt 1080
138          ccaggtggct tagttcgaat tggagaaaga gaaggagaac tttttatcga aaatagctgt 1140
139          agctcagagg aacaagaaaa actagcccag tctttttctg acaatgccag tcgcaaggtc 1200
140          aagggtctg gtatggggct ctttgtggtt aagagtctat tagaacatga aaaattagct 1260
141          tatcgtttcg agatggagga gaatagttta accttcttta tagattttcc aaaagtcgtc 1320
142          caagactag                                                        1329
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151                         20                  25                  30
152         Phe Pro Ser Thr Tyr Leu Ser His Arg Gln Glu Thr Ile Gly Gln Lys
153                     35                  40                  45
154         Ala Thr Ala Ile Ala Gln Ser Leu Glu Gly Lys Asp Arg Gln Ser Ile
155              50                  55                  60
156         Glu Gln Val Leu Asp Leu Tyr Ser Gln Thr Ser Asp Ile Lys Gly Thr
157          65                  70                  75                  80
158         Val Lys Gly Glu Met Thr Glu Asp Lys Leu Glu Val Lys Asp Ser Leu
159                         85                  90                  95
160         Pro Leu Asp Thr Asp Arg Gln Thr Thr Ser Leu Phe Ile Glu Glu Arg
161                         100                 105                 110
162         Glu Val Lys Thr Gln Asp Gly Gly Thr Met Ile Leu Gln Phe Leu Ala
163                     115                 120                 125
164         Ser Met Asp Leu Gln Lys Glu Ala Glu Gln Ile Ser Leu Gln Phe Leu
165              130                 135                 140
166         Pro Tyr Thr Leu Leu Ala Ser Phe Leu Ile Ser Leu Leu Val Ala Tyr
167          145                 150                 155                 160
168         Ile Tyr Ala Arg Thr Ile Val Ala Pro Ile Leu Glu Ile Lys Arg Val
169                     165                 170                 175
170         Thr Arg Arg Met Met Asp Leu Asp Ser Gln Val Arg Leu Arg Val Asp
171                     180                 185                 190
172         Ser Lys Asp Glu Ile Gly Asn Leu Lys Glu Gln Ile Asn Ser Leu Tyr
173                     195                 200                 205
174         Gln His Leu Leu Thr Val Ile Ala Asp Leu His Glu Lys Asn Glu Ala
175              210                 215                 220
176         Ile Leu Gln Leu Glu Lys Met Lys Val Glu Phe Leu Arg Gly Ala Ser
177          225                 230                 235                 240
178         His Glu Leu Lys Thr Pro Leu Ala Ser Leu Lys Ile Leu Ile Glu Asn
179                     245                 250                 255
180         Met Arg Glu Asn Ile Gly Arg Tyr Lys Asp Arg Asp Gln Tyr Leu Gly
181                     260                 265                 270
182         Val Ala Leu Gly Ile Val Asp Glu Leu Asn His His Val Leu Gln Ile
183              275                 280                 285
184         Leu Ser Leu Ser Ser Val Gln Glu Leu Arg Asp Asp Arg Glu Thr Ile
185              290                 295                 300
186         Asp Leu Leu Gln Met Thr Gln Asn Leu Val Lys Asp Tyr Ala Leu Leu
187          305                 310                 315                 320
188         Ala Lys Glu Arg Glu Leu Gln Ile Asp Asn Ser Leu Thr His Gln Gln
189                     325                 330                 335
190         Ala Tyr Leu Asn Pro Ser Val Met Lys Leu Ile Leu Ser Asn Leu Ile
191                     340                 345                 350
192         Ser Asn Ala Ile Lys His Ser Val Pro Gly Gly Leu Val Arg Ile Gly
193                     355                 360                 365
194         Glu Arg Glu Gly Glu Leu Phe Ile Glu Asn Ser Cys Ser Ser Glu Glu
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195                   370              375              380
196      Gln Glu Lys Leu Ala Gln Ser Phe Ser Asp Asn Ala Ser Arg Lys Val
197      385                   390              395              400
198      Lys Gly Ser Gly Met Gly Leu Phe Val Val Lys Ser Leu Leu Glu His
199                   405              410              415
200      Glu Lys Leu Ala Tyr Arg Phe Glu Met Glu Glu Asn Ser Leu Thr Phe
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203                   435              440
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207  <213> ORGANISM: Streptococcus pneumoniae
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211      tctagctatg aggtggccct ggttttactg gatatccaga tgcccaagct caacggctta 180
212      gaagtcctag ctgagattcg taaaaccagt caggttcctg tcttgatgtt gacagctttt 240
213      caagatgagg aatacaagat gagtgccttt gcctctttgg cagatggcta tctggaaaaa 300
214      cctttctccc tctccctttt aaaagtgagg gtggacgcga ttttcaagcg ctactacgat 360
215      acaggacgaa tcttttctta caaggatacc aaggtggact ttgaaagcta cagtgcaagc 420
216      ctcgcaggtc aagaagtgcc tatcaatgcc aaagagttgg aaattctgga ctatctagtg 480
217      aaaaatgaag gccgggcctt gactcgatct cagattatcg atgccgtctg gaaagcgaca 540
218      gatgaggttc cctttgaccg tgttattgat gtttatatca aggaattgcg gaaaaagcta 600
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222  <212> TYPE: PRT
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227      Ser Asp Tyr Leu Thr Asp Cys Gly Tyr Glu Thr Ile Glu Ala Ala Asp
228                   20                  25                  30
229      Gly Gln Glu Ala Leu Glu Gln Phe Ser Ser Tyr Glu Val Ala Leu Val
230                   35                  40                  45
231      Leu Leu Asp Ile Gln Met Pro Lys Leu Asn Gly Leu Glu Val Leu Ala
232                   50                  55                  60
233      Glu Ile Arg Lys Thr Ser Gln Val Pro Val Leu Met Leu Thr Ala Phe
234       65                  70                  75                  80
235      Gln Asp Glu Glu Tyr Lys Met Ser Ala Phe Ala Ser Leu Ala Asp Gly
236                   85                  90                  95
237      Tyr Leu Glu Lys Pro Phe Ser Leu Ser Leu Leu Lys Val Arg Val Asp
238                   100                 105                 110
239      Ala Ile Phe Lys Arg Tyr Tyr Asp Thr Gly Arg Ile Phe Ser Tyr Lys
240                   115                 120                 125
241      Asp Thr Lys Val Asp Phe Glu Ser Tyr Ser Ala Ser Leu Ala Gly Gln
242                   130                 135                 140
243      Glu Val Pro Ile Asn Ala Lys Glu Leu Glu Ile Leu Asp Tyr Leu Val
244                   145                 150                 155                 160
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

Line	?	Error/Warning	Original Text
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863	W	"N" or "Xaa" used: Feature required	Lys Arg Pro Xaa Arg Asp Tyr
914	W	"N" or "Xaa" used: Feature required	Met Xaa Xaa Xaa Xaa Xaa Asn Val Leu Ser X
916	W	"N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Asn
1028	W	"N" or "Xaa" used: Feature required	Xaa Ser Gly Gly Xaa